

Running Head: Coloniality, stochasticity, and phenology

Rethinking ‘normal’: The role of stochasticity in the phenology of a synchronously breeding seabird

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SUMMARY/ABSTRACT

1. Phenological changes have been observed in a variety of systems over the past century. There is concern that, as a consequence, ecological interactions are becoming increasingly mismatched in time, with negative consequences for ecological function.
2. Significant spatial heterogeneity (inter-site) and temporal variability (inter-annual) can make it difficult to separate intrinsic, extrinsic, and stochastic drivers of phenological variability. The goal of this study was to understand the timing and variability of breeding phenology of Adélie penguins under fixed environmental conditions, and to use those data to identify a ‘null model’ appropriate for disentangling the sources of variation in wild populations.
3. Data on clutch initiation were collected from both wild and captive populations of Adélie penguins. Clutch initiation in the captive population was modeled as a function of year, individual, and age to better understand phenological patterns observed in the wild population.
4. Captive populations displayed as much inter-annual variability in breeding phenology as wild populations, suggesting that variability in breeding phenology is the norm and thus may be an unreliable indicator of environmental forcing. The distribution of clutch initiation dates was found to be moderately asymmetric (right skewed) both in the wild and in captivity, consistent with the pattern expected under social facilitation.
5. The role of stochasticity in phenological processes has heretofore been largely ignored. However, these results suggest that inter-annual variability in breeding phenology can arise independent of any environmental or demographic drivers and that synchronous breeding can enhance inherent stochasticity. This complicates efforts to relate

phenological variation to environmental variability in the wild. Accordingly, we must be careful to consider random forcing in phenological processes, lest we fit models to data dominated by random noise. This is particularly true for colonial species where breeding synchrony may outweigh each individual's effort to time breeding with optimal environmental conditions. Our study highlights the importance of identifying appropriate null models for studying phenology.

Keywords: Antarctica, Adélie penguin, Bayesian hierarchical model, climate change, coloniality, phenological mismatch, Pygoscelis adeliae, stochasticity, synchrony

INTRODUCTION

There is concern that ecological interactions are becoming increasingly mismatched in time as a result of climate change-driven shifts in the timing of key life history events such as migration, foraging, and breeding (Thackeray et al. 2016). Such mismatches may result in decreased fitness (Cushing 1974, Visser and Both 2005) with long-term repercussions for population dynamics (Ludwig et al. 2006, Miller-Rushing et al. 2010, McLean et al. 2016). These asynchronies have been observed in a diverse range of taxa, including arthropods (Winder and Schindler 2004, Both et al. 2009), birds (Both et al. 2009, Visser et al. 2012), fish (Durant et al. 2005), and mammals (Post and Forchhammer 2008) and in a variety of ecological systems (Kerby et al. 2012 and references therein). To better understand and predict how phenological change might impact ecological systems, it is important to recognize what factors drive the timing of these life-history events.

Photoperiod has been identified as a proximate driver of the timing of key life history events in both plants and animals (animal breeding, animal migration, plant flowering; Hay 1990, Temte and Temte 1993, Bradley et al. 1999, Helm 2009, Zerbe et al. 2012). Studies of phenological variation (inter-annual variation and/or long-term trends), however, have focused on abiotic environmental factors such as temperature and precipitation (Visser et al. 2009, Thackeray et al. 2016), or biotic factors such as body condition, which may reflect environmental conditions and/or prey availability (Bêty et al. 2003; see review in Dawson 2008). Variability in population-level phenology arises by some combination of three factors: (1) extrinsic drivers: changes in environmental (both abiotic and biotic) conditions, including changes in other components of the ecological community (e.g., prey, predators, mutualists); (2) intrinsic drivers: fixed differences among individuals coupled with demographic turnover within

the population; and (3) stochastic variation: seemingly random variation in the timing of breeding of individuals (unrelated to known intrinsic or extrinsic factors) that propagates up to population-level metrics of phenology. Consistent with usage by Lande et al. (2003), we define stochasticity in this context as variability that is either truly random or, at least, appears random with respect to factors relevant to the question of interest. While numerous studies have focused on intrinsic and extrinsic drivers of phenology, there has been relatively little attention paid to the role of stochasticity. This lack of attention to stochastic factors is due, in part, to the fact that wild populations are subject to fluctuating environmental conditions, making it difficult to identify forces independent of measureable extrinsic and intrinsic factors.

The scale on which data are collected (i.e., population-level vs. individual-level) also contributes to the challenge of identifying stochasticity. Most studies of phenology in wild populations use population-level summary statistics (such as first or mean timing of a life-history event in a population) due to difficulties associated with collecting individual-level data. Metrics that capture the first instance of an event of interest are known to be problematic due to their sensitivity to population size and sampling frequency (Miller-Rushing et al. 2008). While more robust to these influences, population mean metrics can be affected by other factors such as age (Ainley et al. 1983, Ainley 2002) and random variation among individuals (Crawley and Akhteruzzaman 1988) that, through shifts in demographic composition, can impact population-level statistics. For instance, if older individuals breed earlier, an aging population will display an apparent trend towards earlier breeding (Lewis et al. 2012). Similarly, any random subset of individuals may, by chance, have an earlier or later average phenology than another such random subset of individuals.

Individual-level data, in either wild or captive populations, allows us to track the role of demographic turnover (age and individual effects) on phenological response. An even more comprehensive understanding of the role for stochastic factors in driving phenological variability can be developed by paring studies of wild populations with studies of populations under fixed environmental conditions (Lambrechts et al. 1999, Dunne et al. 2003, Visser et al. 2009). Phenological variability in captive populations kept under fixed conditions represents a null model against which interannual variability in wild populations can be compared. Without such a control group, it may be difficult to determine the extent to which phenological variability is driven by environmental variability or, alternatively, inherent stochasticity. An estimate of interannual variation under fixed environmental conditions is therefore of value when interpreting phenological studies of wild populations. Assessing variability under these conditions may be particularly important for colonially breeding species that may rely on social cues to synchronize breeding (Ims 1990b).

Here we used data collected from both wild (representing naturally variable environmental conditions) and captive (representing fixed environmental conditions) populations of Adélie penguins *Pygoscelis adeliae*, to identify the role of stochastic factors in driving breeding phenology. Adélie penguins are a site faithful, highly colonial species that inhabit the Antarctic continent and surrounding islands. Several studies (Barbraud and Weimerskirch 2006, Emmerson et al. 2011, Hinke et al. 2012, Lynch et al. 2012, Youngflesh et al. 2017) have sought to understand the conditions associated with breeding phenology in Adélie penguins. However, despite considerable effort to collect and analyze long-term phenological data, our understanding of what drives phenology in this species and the potential role that stochastic factors might play, is limited. Our aim was to address three principal questions in this study: 1) how variable is

Adélie penguin breeding phenology in the absence of environmental variability; 2) can variation in breeding phenology under fixed environmental conditions be explained by individual variation and age structure, or is there substantial residual random variation that remains unexplained; and 3) what implications do our findings have for interpreting variability in wild populations of synchronously breeding colonial species? In sum, to what extent have we been overemphasizing the role of exogenous environmental forcing in the phenological variability of some wild populations?

MATERIALS AND METHODS

Description of data

Individual-level data on clutch initiation date (CID – the date in which the first egg is laid in each nest) were obtained for all individuals in a captive Adélie penguin population at SeaWorld San Diego from 1992 - 2015 (89 penguins in total). The number of breeding females in each year varied from 12 to 37 throughout the course of the study. The youngest birds to breed were 2 years of age, while the oldest were 45 years of age. Most penguins (67 of the 89) were born in captivity – individuals born before 1984 were taken as chicks from wild populations in the Ross Sea region of Antarctica in 1976.

All captive penguins were associated with unique identifiers, and metrics for each individual were tracked through time. Temperature at the facility was kept at a constant -4°C to -2°C year-round. Feeding regime of the captive birds did not change over the study period. Nesting materials (stones) were provided at the same time in each year. Photoperiod for the exhibit

lighting mimicked that of 77°S latitude (though minimal exhibit lighting is required during the winter period), representative of the southern limit of the Adélie penguin breeding range. Seasonal variations in lighting are accounted for in the lighting regime and are constant from year to year. The viewing area is setup in such a way to minimize light exposure to the penguin enclosure. The penguin exhibit at SeaWorld underwent a 6-month renovation in 2005. The captive penguin population used in this study was kept in a separate enclosure during this renovation, which may have impacted breeding phenology in this year.

Data on CID were also obtained for a unique set of 100 individuals each year in a wild population of Adélie penguins located at Admiralty Bay, Antarctica (62.2°S, 58.4°W) from 1986-2012 using methodologies outlined in Hinke et al. (2012). Individual-level data across years was not available for the wild population. Wild penguins are typically younger than those in captivity, generally less than 20 years of age (Ainley et al. 1983, Ainley 2002).

Statistical analysis of individual phenology in marked captive penguins

For the captive Adélie penguin time series, a hierarchical Bayesian approach was used to model CID (y_{ij}), with year (i) and individual (j) as random effects (α and β , respectively) and age as a fixed effect (γ):

$$y_{ij} = \mu + \alpha_i + \beta_j + \gamma * AGE_{ij} + \varepsilon_{ij} \quad (1)$$

$$\alpha_i \sim N(0, \sigma^2_{year})$$

$$\beta_j \sim N(0, \sigma^2_{individual})$$

$$\varepsilon_{ij} \sim N(0, \sigma^2_{model})$$

where μ represents the intercept, AGE represents the age of the female, and ε represents the error term. This model was used to determine whether variation in y_{ij} was driven by the α parameter (variance attributed to a colony-wide effect that varies among years), the β parameter (variance attributed to fixed differences between individuals), the AGE covariate, or the error term (ε). Individual data used in this statistical framework allowed us to account for potential confounding factors related to differences in phenology due to individual identity (or quality) and age, and provide a more complete understanding of these processes than is possible using population-level summary statistics.

Models were fit using the R package ‘rjags’ (Plummer 2013), an interface to JAGS (Plummer 2003), in the R statistical environment (R Core Team 2016). Normal priors were used for α , β , γ , and ε . Broad Gamma priors were used for all precision ($\tau = \frac{1}{\sigma^2}$) parameters (shape = 0.01, rate = 0.01). Posterior distributions were derived from three chains with 5,000 samples (after thinning every other draw) following a ‘burn-in’ period of 40,000 draws and an adaptation period of 5000 draws. Model convergence was assessed through a visual analysis of the posterior chains, in addition to the use of the Gelman-Rubin convergence diagnostic (Brooks and Gelman 1998). All models unambiguously converged. Parameter estimate plots were generated using the ‘MCMCvis’ package (Youngflesh 2016) while other plots were generated using the ‘ggplot2’ package (Wickham 2009) in the R statistical environment.

Statistical analysis of population-level phenology in captive and wild penguins

No information on individual phenology across years was available for the wild population (i.e., no information on the β parameter or AGE covariate), leaving it ambiguous as to which component was contributing to the variability in y_{ij} (CID of individual j in year i). Therefore, to

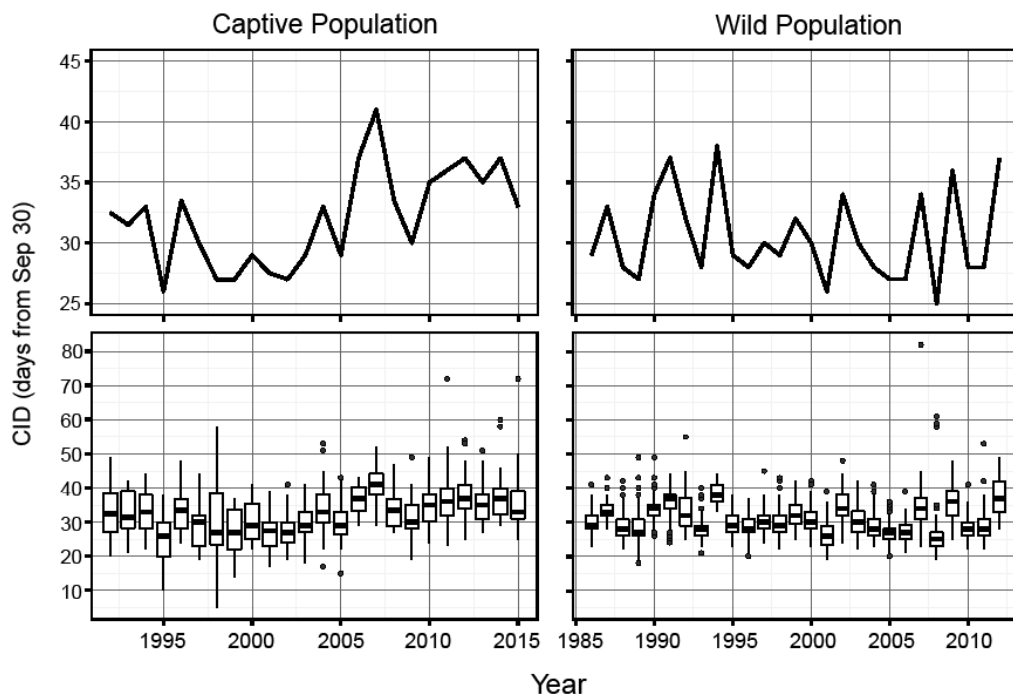
directly compare the captive and wild Adélie populations, we considered population-level aggregate summaries of phenology in both populations. The median colony CID in each year (median across individuals; denoted $y_{i\cdot}$) was calculated for both the captive and wild Adélie penguin populations. Between year variation in median phenology, $\sigma_{between}^2 = var(y_{i\cdot})$, included variation from all sources (year, individual, age, and unexplained variance as captured by ε). Note that in contrast to σ_{model}^2 in Eq 1, $\sigma_{between}^2$ includes variation due to age and individual identity as well as residual stochastic variation unrelated to these factors. For both the captive and wild populations, variation within year i , $\sigma_{i,within}^2 = var(y_{ij})$, was used as a measure of year-specific, within-population breeding synchrony. We also note that while differences in (simulated) latitude may have generated a fixed difference in photoperiod between the captive and wild populations, our analysis examined only within-site inter-annual variability in breeding phenology.

To investigate whether individual breeding dates within a colony were distributed symmetrically around a population mean, as might be expected *a priori* if individuals were acting independently, CID values in each year were standardized ($z_{i\cdot} = \frac{y_{i\cdot} - \bar{y}_{i\cdot}}{sd(y_{i\cdot})}$) and aggregated across years to be analyzed for skewness using a D'Agostino skewness test (D'Agostino 1970). All analyses were performed in the R statistical environment (R Core Team 2016).

RESULTS

Inter-annual and intra-annual variance in CID

218 Inter-annual variance of median colony CID was similar between the captive
 219 ($\sigma^2_{between-captive} = 15.8$ [$SE = 4.7$]) and wild ($\sigma^2_{between-wild} = 13.5$ [$SE = 3.7$]) populations
 220 (Fig. 1). This degree of phenological variability is comparable to that seen in other taxa
 221 (Appendix S1). Within year, individual birds were relatively synchronous in both populations,
 222 with greater synchrony among individuals in the wild population compared to the captive
 223 population ($E[\sigma^2_{within-wild}] < E[\sigma^2_{within-captive}]$; Welch two-sample t-test, $t = 4.99$, $df = 28.5$, p
 224 < 0.001) (Fig. 1; Appendix S1).



225
 226 **Fig. 1.** Mean colony breeding phenology (top panels) and distribution of individual CID in each
 227 year (bottom panels). The bold lines in the box-and-whisker plots represent the median CID
 228 while boxes represent the 25th and 75th quantiles. The top and bottom of the whiskers are $1.5 \times$
 229 IQR (inter-quartile range) from the upper and lower boxes, respectively. Data beyond this range

are plotted as points. The number of data points per year in the captive population ranged from 13 to 38. One hundred data points were collected for each year in the wild population.

Individual phenology in marked captive penguins

A strong year effect (α) on CID was apparent for the captive penguin population (Fig. 2a; $median(\sigma_{year}^2) = 13.81$ [Appendix S1]). Significant year to year variation was found, even when accounting for the effects of age and individual. Inter-annual variation is still substantial when accounting for first-order autocorrelation (Appendix S2). Random effects due to individual (β) were notable (as evidenced by the spread of β parameter estimates), with some individuals breeding consistently earlier/later than other individuals (Fig. 2b; $median(\sigma_{individual}^2) = 13.66$ [Appendix S1]). Over the 24-year study period, 16 different individuals were the first to lay eggs in a particular year (in 3 of these years, multiple individuals laid eggs on the same day). No biologically significant effect of age (γ) on CID was found (median posterior estimate = 0.06 days/year); the 95% credible interval overlapped 0 (Fig. 2c). Variance unaccounted for by the model is represented by $median(\sigma_{model}^2) = 34.96$ (Appendix S1).

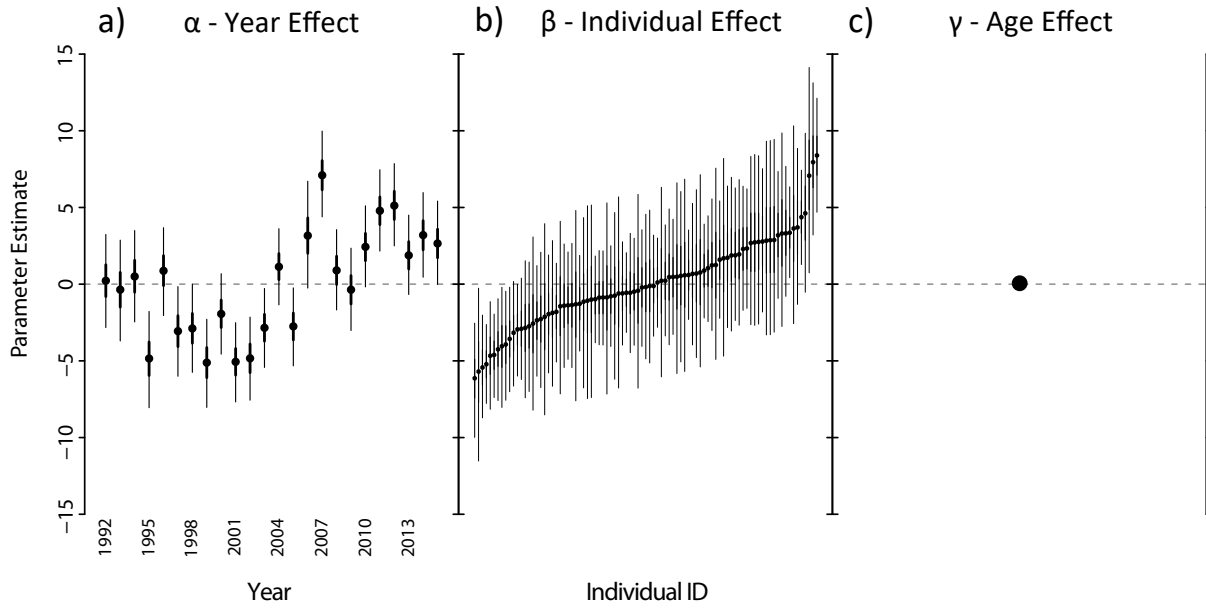


Fig. 2. Posterior estimates for the captive population parameters: (a) year effect – α ; (b) individual effect – β ; and (c) age effect – γ parameters (see Eq 1). Black circles represent posterior medians. Thicker lines represent 50% credible intervals while thinner lines represent 95% credible intervals. Error bars for the γ parameter are obscured by the point itself.

Intra-annual variance in CID

The distributions of CID for both captive and wild populations (Fig. 3) had a small but statistically significant right skew ($g_1^{captive} = 0.54$ [SE = 0.10]; $g_1^{wild} = 0.79$, [SE = 0.04]; D'Agostino test, $p < 0.001$).

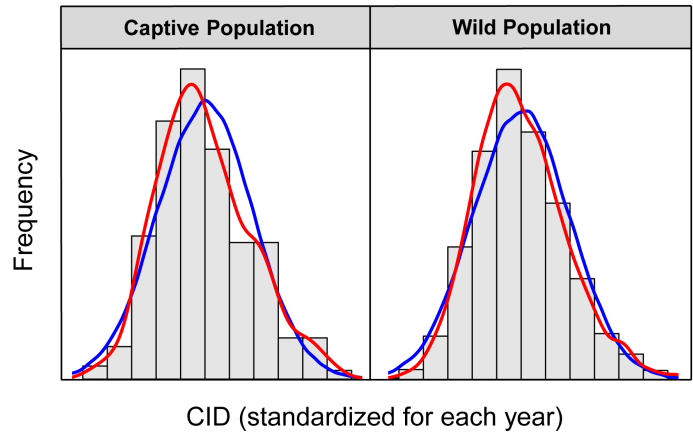


Fig. 3. Distribution of CIDs for the captive (left) and wild (right) populations. Data were standardized and aggregated across years. Colored lines depict the kernel density estimates on the distribution. Red lines represent the actual distributions of CID, while the blue lines represent the normal distributions generated using the actual mean and variance of the CID distribution.

DISCUSSION

Despite prior expectations of lower inter-annual variance in breeding phenology under fixed environmental conditions, we found that both the captive and wild Adélie penguin populations exhibit a similar degree of inter-annual fluctuation in breeding phenology. Stochasticity appears to play a substantial role in determining the timing of Adélie penguin breeding within the window of time dictated by biological and physical constraints. We suggest that stochasticity at the individual level is amplified by the importance of breeding synchrony among individuals, producing the observed inter-annual variance.

Inherent inter-annual variation

Previous studies have suggested that photoperiod (Dawson 2008), abiotic conditions such as rainfall (Leitner et al. 2003, Deviche et al. 2006) and temperature (Both et al. 2004, Torti & Dunn 2005, Visser et al. 2009), biotic conditions such as food availability (Reynolds et al. 2003), or some combination of these factors, are important in regulating phenology in a number of bird species. While these conditions may define a larger envelope of time in which successful breeding may occur, our analysis of a captive Adélie penguin population shows that external drivers neither explain nor are required to generate substantial inter-annual variability in breeding phenology (i.e., a large year effect). Inter-annual fluctuations are apparent even under constant environmental conditions and after accounting for the effects of individual variation and age (Fig. 2a). Other potential factors that we thought might have influenced penguin breeding phenology, such as number of breeders in a given season, the timing of nesting material availability, and potential effects of the 2005 captive population exhibit renovation, were investigated but ultimately determined to have only minor effects (Appendix S2).

Beyond the random effect of year, some fixed differences in the timing of breeding among individuals in the captive population do exist – that is, some individuals breed earlier than others on average (Fig. 2b). However, the relatively minor shifts in the composition of the population each year cannot explain the inter-annual fluctuations in the breeding phenology of captive individuals. While previous work has suggested that age plays a role in determining Adélie penguin breeding phenology in the wild (Ainley et al. 1983, Ainley 2002), the effect of age on breeding phenology was minimal in the captive population studied here (Fig. 2c). This is not surprising, given that one hypothesized mechanism by which age might impact breeding phenology is through an individual's ability to navigate back to the breeding colony following the overwintering period. Older individuals, being more experienced, are thought to be able to

find their way back to the breeding colonies more quickly, particularly through substantial sea ice (Ainley et al. 1983). With no migration in a captive population, we would expect age and experience to have a substantially smaller impact on breeding phenology.

Interplay between synchrony and stochasticity

Adélie penguins are highly synchronous breeders within a population in a given season (Fig. 1; see also Ainley 2002), and previous work has shown that increased synchrony among individuals leads to increased breeding success (Youngflesh et al. 2017). Where colonial breeding is driven by predator avoidance, individuals that breed not only in the same area but also at the same time as others in the population would be at an advantage (Darling 1938, Young 1994). Penguins breeding during the same time period in the same location can more easily defend nests against aerial predators, a principal threat to Adélie penguin chicks (Young 1994). Synchronous breeding also results in an overwhelming influx of potential prey resources for species that prey on penguins; such ‘predator-swamping’ can facilitate higher breeding success (Ims 1990a). We hypothesize that the fitness consequences of breeding in sync with conspecifics may outweigh the importance of matching optimal environmental conditions within the environmentally-driven time envelope in which reproduction can occur successfully (as suggested in Hinke et al. 2012, Youngflesh et al. 2017). We suggest that the importance of this phenomenon for any given species reflects a balance between the expected fitness advantages of synchronous breeding among conspecifics and the fitness advantages of breeding during some (environmentally-determined) optimal period of time – the latter of which may be more difficult to assess for an individual with limited information.

In this way, predators indirectly influence the breeding phenology of Adélie penguins – a top-down process. Abiotic (e.g., photoperiod, temperature) and/or bottom-up processes (e.g., resource availability, organism physiological condition) are typically the focus of phenological studies. However, top-down forcing (via antagonists such as predators and pathogens) has been identified as an important process in the regulation of a number of phenological processes, including absolute phenology (Elzinga et al. 2007, Galloway and Burgess 2012), phenological synchrony (Hatchwell 1991, Sinclair et al. 2000), and the rate at which offspring develop (Vonesh 2005). These processes often operate in concert with abiotic and/or bottom-up processes (as suggested by Varpe et al. 2007, Burr et al. 2016), painting a complex picture of multiple ecological determinants of phenological processes. While the mechanisms for top-down control on phenology are diverse, these patterns may be more common among colonial breeders given the importance of phenological synchrony for predator avoidance in many species (Ims 1990b).

While the precise mechanism that regulates this highly synchronous behavior in Adélie penguins is unknown, social cues have been found to drive courtship and copulation (Waas 1988, 1991, 1995, Waas et al. 2000), and result in more synchronized breeding patterns (Setiawan et al. 2007). This has been demonstrated in a number of birds (Burger 1979, Danchin 1988, Waas et al. 2005), including other species of penguins, as well as in mammals (McClintock 1978, Scott 1986, Berger 1992). Vocalizations (Clark et al. 2012), exposure to courtship displays (Lehrman and Friedman 1969), and chemical cues (McClintock 1978) have all been demonstrated as proximate behavioral mechanisms by which this social facilitation occurs.

Slightly right skewed distributions of CID are apparent within each year – very late breeders in this right skewed distribution contribute to a relatively large residual variance in our model. This skew is also consistent with, though by no means proves conclusively, a role for social

facilitation in the timing of breeding. Even a simple model in which breeding is accelerated proportional to the number of pairs that have recently initiated breeding creates a right skewed distribution for clutch initiation (Appendix S1). This notion of facilitation is further supported by the strong relationship (70% of variance explained) between first CID (the first breeders in each year) and median CID in both the captive and wild populations (Appendix S1). Right skewed distributions of phenological events are apparent in many species of both birds and plants (Thomson 1980, Sparks et al. 2005, Wilson 2013) in magnitudes similar to those observed here (Appendix S1). Environmental factors may play a role in driving this pattern for many species, a hypothesis difficult to exclude if only wild data were available. In this case, however, both a right skewed distribution and a strong relationship between first breeding and median breeding are apparent under controlled conditions, despite inter-annual variability in the overall timing of breeding.

It should be noted that the captive penguin population in this study exhibited less synchrony among individuals in a given year than did the wild population (Fig. 1; Appendix S1). One possible explanation for this relates to colony size; larger populations in the wild may, through increased colony noise, better facilitate the transmission of social cues (Waas et al. 2000). Other possibilities include the notion that the degree of synchrony is a plastic trait that may be relaxed under the predator-free conditions of captivity. Future work, including manipulative experiments, is required to understand the precise behavioral mechanisms regulating synchrony in this species.

To be clear, we are not suggesting that synchronous breeding is necessary to observe the impacts of stochastic factors on breeding phenology at the individual level, but rather that the importance of synchrony in colonial species may facilitate the propagation of stochasticity from

the individual-level to that of the population. Social cues that facilitate synchrony (see above) may encourage individuals to initiate breeding once other individuals in the colony have done so. This cascading effect of synchronous breeding may drive a shift in the average phenology of the population that is largely uncoupled from any environmental trigger.

In ignoring the role of stochasticity, have we been modeling noise?

In the search for causal drivers for phenology, the role of inherent stochasticity has been largely ignored in the existing phenological literature. Our study has important implications for studying patterns of phenology across all animal systems as it highlights the difficulty of teasing out the extent to which the environment may, or may not, be driving variation in phenology. The observed levels of inter-annual variability under fixed environmental conditions are of a similar magnitude to those seen in the wild (Fig. 1; Appendix S1, S2) – a surprising result. Previous studies of Adélie penguin phenology at Admiralty Bay found October mean air temperature (thought to be related to snow melt and nest site availability) to be the most important environmental determinant of CID in a model selection framework (Hinke et al. 2012, Lynch et al. 2012). Our analyses of the same CID data (with additional years beyond what was used in the original studies) do not contradict these original findings, but suggest that environmental drivers, such as temperature, are layered on top of substantial ‘built in’ variability. Put another way, our null model for phenological studies should not, by default, be one of stasis.

Whether the drivers that influence a pair’s ‘decision’ to breed are unknown, or unknowable, the implication is that phenological variability of this scale can be generated in the absence of environmental variability. This finding is of practical importance, as it highlights the difficulty in identifying external causal drivers of phenological events. Our study shows that stochastic

variation in penguin breeding phenology, with respect to the environmental factors addressed here, may be the rule rather than the exception and does not require external forcing from the environment. This is similar to stochastic outcomes of individuals, whereby identical individuals, experiencing identical conditions, will differ with respect to lifespan and fecundity (Caswell 2011). This role of stochasticity may partially explain previous findings of a relatively weak relationship between Antarctic seabird breeding phenology and environmental forcing (Barbraud and Weimerskirch 2006).

One way to address the inherent convolution of environmental variability and inherent stochasticity is through the study of captive populations in controlled conditions. While studies focusing on plants more often include experiments in controlled environments to distinguish the role of multiple factors on phenology (Cleland et al. 2007), there are fewer studies elucidating inter-annual changes in phenology in captive animals (but see Lambrechts et al. 1999, Visser et al. 2009). Captive animal populations are not, of course, perfect replicas of wild populations. For instance, penguins in captive populations are kept in enclosed spaces and do not undergo an overwinter migration. Captive populations are also limited in size, often smaller than what might be observed in the wild. Accordingly, we must be cautious not to overextend the analogy between captive and wild populations. Nevertheless, studies focusing on populations in controlled conditions can provide a wealth of information on phenology in the absence of all environmental factors deemed potentially important in wild populations. Identification and tracking of individual animals further allows for straightforward estimation of age effects and random individual variation. Ultimately these studies can provide a reasonable null model against which to assess factors contributing to variation in wild populations. Studies involving experimental manipulation and/or transplantation of organisms to new environments (e.g., Helm

2009) may provide additional power to disentangle the factors controlling breeding phenology. Our study highlights the challenges of understanding the factors driving phenology in wild populations, and reminds us to take caution in ascribing causality when we are unaware of the degree of inherent variation in the response variable of interest.

AUTHORS' CONTRIBUTIONS

CY, HJL, and SJ conceived the ideas and designed the methodology; JTH, LD, JSL, WZT, and SGT collected the data; CY analyzed the data; CY and HJL led the writing of the manuscript. All authors contributed to drafts and gave final approval for publication.

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DATA ACCESSIBILITY

426 Data used in this study are available from the Dryad Digital Repository
427 <https://doi.org/10.5061/dryad.23sv1> (Youngflesh et al. 2017).

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Appendix S1: Study R/JAGS code with results

Rethinking ‘normal’: The role of stochasticity in the phenology of a synchronously breeding seabird

Casey Youngflesh, Stephanie Jenouvrier, Jefferson T. Hinke, Lauren DuBois, Judy St. Leger, Wayne Z. Trivelpiece, Susan G. Trivelpiece, Heather J. Lynch

Initial set up

Packages

```
#install packages if they don't exist - then load them
if('pacman' %in% rownames(installed.packages()) == FALSE)
{
  install.packages('pacman')
}

pacman::p_load(ggplot2,
               reshape2,
               dplyr,
               rjags,
               moments,
               MCMCvis)
```

Inter-annual variation in CID

Load data

```
setwd('Data')

captive_data <- read.csv('Captive_CID.csv', header = TRUE)
wild_data <- read.csv('Wild_CID.csv', header = TRUE)
```

Function to calculate intra-annual median and var

```
srt.fun <- function(IN)
{
  #IN <- SD_lay
  yrs <- unique(IN$YEAR)

  OUT <- c()
  for(i in min(yrs):max(yrs))
  {
    #i <- 1993
    temp <- filter(IN, YEAR == i)
    t_md <- median(temp$J_CID)
    t_var <- var(temp$J_CID)
    temp2 <- data.frame(YEAR = i, MEDIAN = t_md, VAR = t_var)
    OUT <- rbind(OUT, temp2)
  }
}
```

```

  return(OUT)
}

```

Function to calculate SE of variance

$$\sigma_{s^2} = s^2 * \sqrt{2/(n-1)}$$

```

se_var <- function(data)
{
  OUT <- var(data)*sqrt(2/(length(data)-1))
  return(OUT)
}

```

Captive inter-annual variance - $var(y_{i.})$

```

captive_md_sd <- srt.fun(captive_data)

(c_med <- var(captive_md_sd$MEDIAN))

```

```
## [1] 15.83288
```

Captive standard error of variance

```
se_var(captive_md_sd$MEDIAN)
```

```
## [1] 4.668862
```

Wild inter-annual variance - $var(y_{i.})$

```

wild_md_sd <- srt.fun(wild_data)

(w_med <- var(wild_md_sd$MEDIAN))

```

```
## [1] 13.49003
```

Wild standard error of variance

```
se_var(wild_md_sd$MEDIAN)
```

```
## [1] 3.741461
```

Inter-annual variation in CID from literature

Inter-annual variation in CID in the Adélie penguin population are of a similar magnitude to those seen in other bird species.

```

setwd('Data')

lit_data <- read.csv('Lit_data.csv', header = TRUE)

```

Both et al. 2009 (Fig. 2) - Blue tit, Great tit, Pied flycatcher, Coal tit, Sparrowhawk

#detrend because we are interested in the interannual variance - trends would confound this estimate

```

fit_BT_B_2009 <- lm(lit_data$BT_B_2009 ~ lit_data$YEAR)
res_BT_B_2009 <- residuals(fit_BT_B_2009)
v_BT_B_2009 <- var(res_BT_B_2009)

fit_GT_B_2009 <- lm(lit_data$GT_B_2009 ~ lit_data$YEAR)
res_GT_B_2009 <- residuals(fit_GT_B_2009)
v_GT_B_2009 <- var(res_GT_B_2009)

```

```

fit_PF_B_2009 <- lm(lit_data$PF_B_2009 ~ lit_data$YEAR)
res_PF_B_2009 <- residuals(fit_PF_B_2009)
v_PF_B_2009 <- var(res_PF_B_2009)

fit_CT_B_2009 <- lm(lit_data$CT_B_2009 ~ lit_data$YEAR)
res_CT_B_2009 <- residuals(fit_CT_B_2009)
v_CT_B_2009 <- var(res_CT_B_2009)

#no need to detrend - no significant change
v_SH_B_2009 <- var(lit_data$SH_B_2009, na.rm = TRUE)

```

Valtonen et al. 2017 (Fig. 2) - Common redstart, Great tit, Pied flycatcher

```

#no need to detrend - no significant change
v_CR_V_2017 <- var(lit_data$CR_V_2017, na.rm = TRUE)

v_GT_V_2017 <- var(lit_data$GT_V_2017, na.rm = TRUE)

v_PF_V_2017 <- var(lit_data$PF_V_2017, na.rm = TRUE)

```

Species	Publication	Metric	Inter-annual Variance
Blue tit	Both et al. 2009	Hatch date	11.94
Great tit	Both et al. 2009	Hatch date	12.82
Pied flycatcher	Both et al. 2009	Hatch date	4.22
Coal tit	Both et al. 2009	Hatch date	25.11
Sparrowhawk	Both et al. 2009	Hatch date	9.74
Common redstart	Valtonen et al. 2017	Clutch initiation date	10.65
Great tit	Valtonen et al. 2017	Clutch initiation date	15.62
Pied flycatcher	Valtonen et al. 2017	Clutch initiation date	10.26
Adélie penguin (captive)	This publication	Clutch initiation date	15.83
Adélie penguin (wild)	This publication	Clutch initiation date	13.49

Adélie penguins exhibit degrees of inter-annual variance in phenology comparable to other species.

Plot median CID over time - Captive

```

plt_t <- data.frame(YEAR = 1992:2015, MD_CID = captive_md_sd$MEDIAN)
plt <- melt(plt_t, id = 'YEAR')

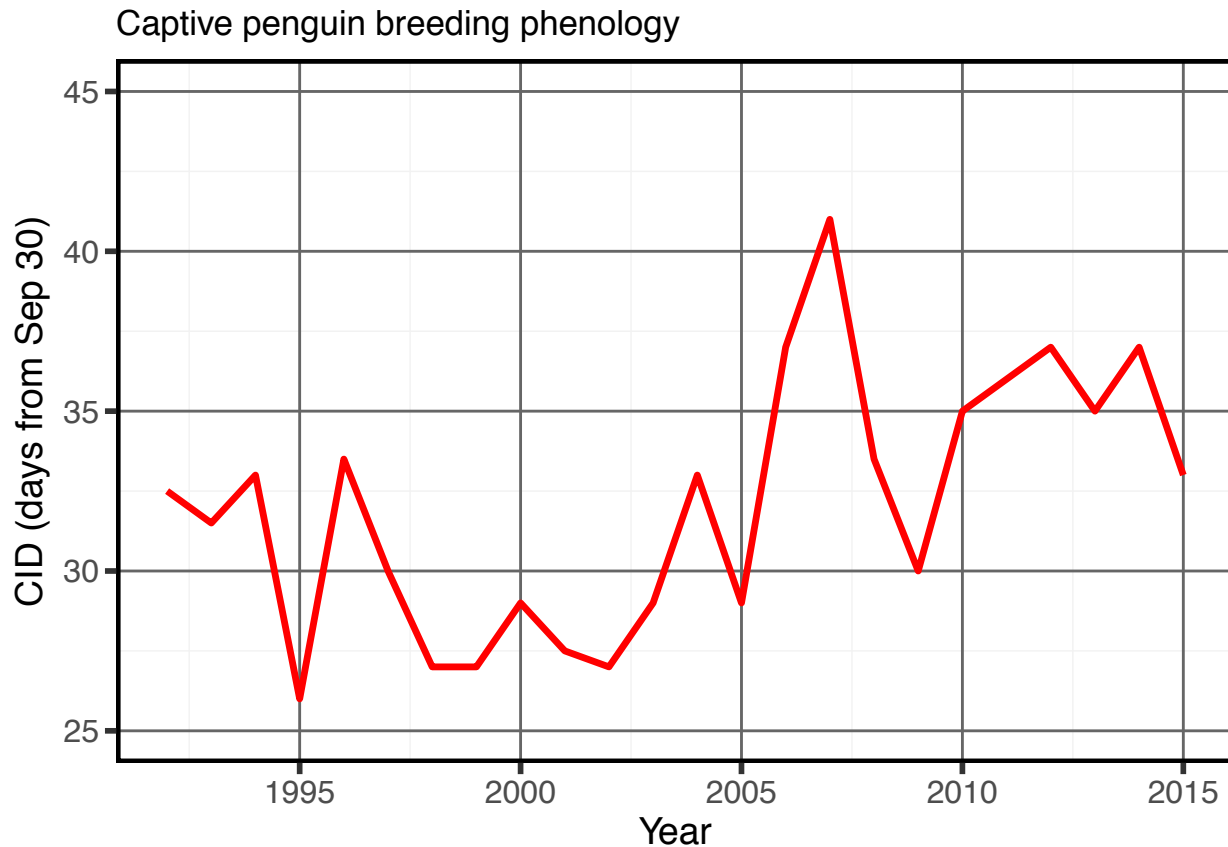
#CAPTIVE PLOT
ggplot(plt, aes(YEAR, value)) +
  geom_line(size = 1.2, col = 'red') +
  theme_bw() +
  ggtitle('Captive penguin breeding phenology') +
  xlab('Year') +
  ylab('CID (days from Sep 30)') +
  coord_cartesian(xlim = c(1990, 2015)) +
  coord_cartesian(ylim = c(25, 45)) +
  scale_x_continuous(breaks = seq(1990, 2015, by = 5)) +
  scale_y_continuous(breaks = c(25, 30, 35, 40, 45)) +

```

```

theme(
  axis.text = element_text(size = 12), #axis label size
  axis.title = element_text(size = 14),
  panel.grid.major = element_line(color = 'gray40'), #lower # is darker
  panel.grid.minor = element_line(color = 'gray95'),
  panel.background = element_blank(),
  panel.border = element_rect(fill = NA, color= 'black', size = 1.5),
  axis.ticks.length= unit(0.15, 'cm'), #length of axis tick
  axis.ticks = element_line(size = 1)
)

```



Plot median CID over time - Wild

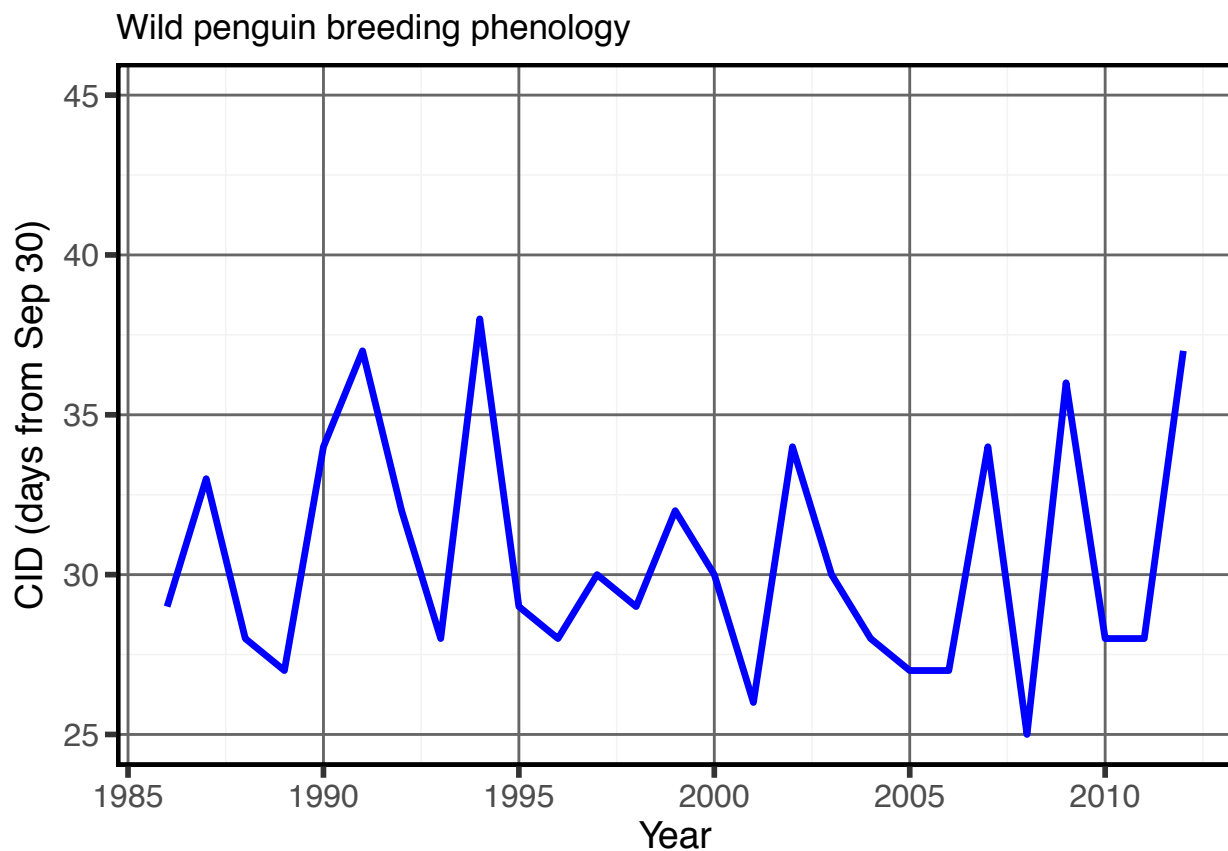
```

plt_t2 <- data.frame(YEAR = 1986:2012, MD_CID = wild_md_sd$MEDIAN)
plt2 <- melt(plt_t2, id = 'YEAR')

#WILD PLOT
ggplot(plt2, aes(YEAR, value)) +
  geom_line(size = 1.2, col = 'blue') +
  theme_bw() +
  ggtitle('Wild penguin breeding phenology') +
  xlab('Year') +
  ylab('CID (days from Sep 30)') +
  coord_cartesian(xlim = c(1984, 2012)) +

```

```
coord_cartesian(ylim = c(25, 45)) +
scale_x_continuous(breaks = seq(1985, 2012, by = 5)) +
scale_y_continuous(breaks = c(25, 30, 35, 40, 45)) +
theme(
  axis.text = element_text(size = 12), #axis label size
  axis.title = element_text(size = 14),
  panel.grid.major = element_line(color = 'gray40'), #lower # is darker
  panel.grid.minor = element_line(color = 'gray95'),
  panel.background = element_blank(),
  panel.border = element_rect(fill = NA, color = 'black', size = 1.5),
  axis.ticks.length = unit(0.15, 'cm'), #length of axis tick
  axis.ticks = element_line(size = 1)
)
```



Determine which female is the first to lay in each year (including ties for first)

```
FEM <- c()
for (i in 1992:2015)
{
  #i <- 1997
  temp <- filter(captive_data, YEAR == i)
  pos <- which(temp$J_CID == min(temp$J_CID))
  t_data <- temp[pos,]
```

```
FEM <- rbind(FEM, t_data)
}
```

16 different 'leaders' in 24 years

```
length(unique(FEM$FEMALE_ID))
```

```
## [1] 16
```

Intra-annual variation in CID

```
#t-test to determine if intra-annual variation differs between captive and wild populations
t.test(captive_md_sd$VAR, wild_md_sd$VAR)
```

```
##
## Welch Two Sample t-test
##
## data: captive_md_sd$VAR and wild_md_sd$VAR
## t = 4.9893, df = 28.488, p-value = 2.733e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 19.51181 46.65717
## sample estimates:
## mean of x mean of y
## 50.75654 17.67205
```

Number of breeders

```
len_fun <- function(IN)
{
  yrs <- range(IN$YEAR)

  LEN <- c()
  for(i in yrs[1]:yrs[2])
  {
    #i <- 1992
    temp <- filter(IN, YEAR == i)
    t1 <- dim(temp)[1]
    tb <- c(i, t1)
    LEN <- rbind(LEN, tb)
  }

  return(LEN)
}
```

```
#range
range(len_fun(captive_data)[,2])
```

```
## [1] 12 37
```

Hierarchical model - captive population

JAGS model

$$y_{ij} = \mu + \alpha_i + \beta_j + \gamma * AGE_{ij} + \epsilon_{ij}$$

$$\alpha_i \sim N(0, \sigma_{year}^2)$$

$$\beta_j \sim N(0, \sigma_{individual}^2)$$

$$\epsilon_{ij} \sim N(0, \sigma_{model}^2)$$

```
setwd('Data')

AGE_mat <- read.csv('AGE_mat.csv', header= TRUE)
CID_mat <- read.csv('CID_mat.csv', header= TRUE)

DATA <- list(
  y = CID_mat,
  yr = 1:NCOL(CID_mat),
  ind = 1:NROW(CID_mat),
  age = AGE_mat,
  N = NCOL(CID_mat), #columns are year in matrix
  M = NROW(CID_mat)) #rows are individuals

#-----#
#model

#alpha = YEAR - random
#beta = INDIVIDUAL - random
#gamma = AGE - fixed

setwd('JAGS')

{
sink("captive.jags")

cat("
  model {

    for(t in 1:N)
    {
      for(i in 1:M)
      {
        y[i,t] ~ dnorm(mu.g[i,t], tau)
        mu.g[i,t] <- mu + alpha[yr[t]] + beta[ind[i]] + gamma*age[i,t]
      }
    }

    #priors
```

```

#year
for(t in 1:N)
{
  alpha[t] ~ dnorm(0, tau.year)
}

#individual
for(i in 1:M)
{
  beta[i] ~ dnorm(0, tau.ind)
}

#mu, gamma, and tau
mu ~ dnorm(0, 0.001)
gamma ~ dnorm(0, 0.001)
tau ~ dgamma(0.01, 0.01)
var.model <- 1/tau #convert from precision to variance

#hyperparameters
tau.year ~ dgamma(0.01, 0.01)
var.year <- 1/tau.year
tau.ind ~ dgamma(0.01, 0.01)
var.ind <- 1/tau.ind

}",fill = TRUE)

sink()
}

```

Run model

```

#-----#
#Starting values

Inits <- function() {list(alpha = rep(rnorm(1),
                                     ncol(CID_mat)),
                          beta = rep(rnorm(1),
                                     nrow(CID_mat)),
                          tau = rgamma(1, 1),
                          mu = rnorm(1),
                          gamma = rnorm(1),
                          tau.year = rgamma(1, 1),
                          tau.ind = rgamma(1, 1))}

#-----#
#Parameters to track

Pars <- c('alpha', 'beta', 'gamma', 'var.year', 'var.ind', 'var.model')

# Inputs for MCMC -----#

```



```

n_adapt <- 5000 # number for initial adapt
n_burn <- 40000 # number burnin
n_draw <- 10000 # number of final draws to make
n_thin <- 2 # thinning rate
n_chain <- 3 # number of chains

Rhat_max <- 1.1 # max allowable Rhat (close to 1 = convergence)
n_max <- 1e7 # max allowable iterations

#-----#
#Run model

jm = jags.model(data = DATA,
                file = "JAGS/captive.jags",
                inits = Inits,
                n.chains = 3,
                n.adapt = n_adapt)

update(jm, n.iter = n_burn)

out = coda.samples(jm,
                  n.iter = n_draw,
                  variable.names = Pars,
                  thin = n_thin)

#extra draws to ensure convergence
n_total <- n_burn + n_draw
n_extra <- 0
while(max(MCMCsummary(out)[,6]) > Rhat_max &
      n_total < n_max)
{
  out <- update(out,
                n.iter = n_draw,
                n.chains = n_chain,
                n.thin = n_thin)

  n_extra <- n_extra + n_draw
  n_total <- n_total + n_draw
}

n_final <- n_draw/n_thin

```

Inferences were derived from 5000 samples drawn following an adaptation period of 5000 draws, and a burn-in period of 4×10^4 draws using 3 chains and a thinning rate of 2.

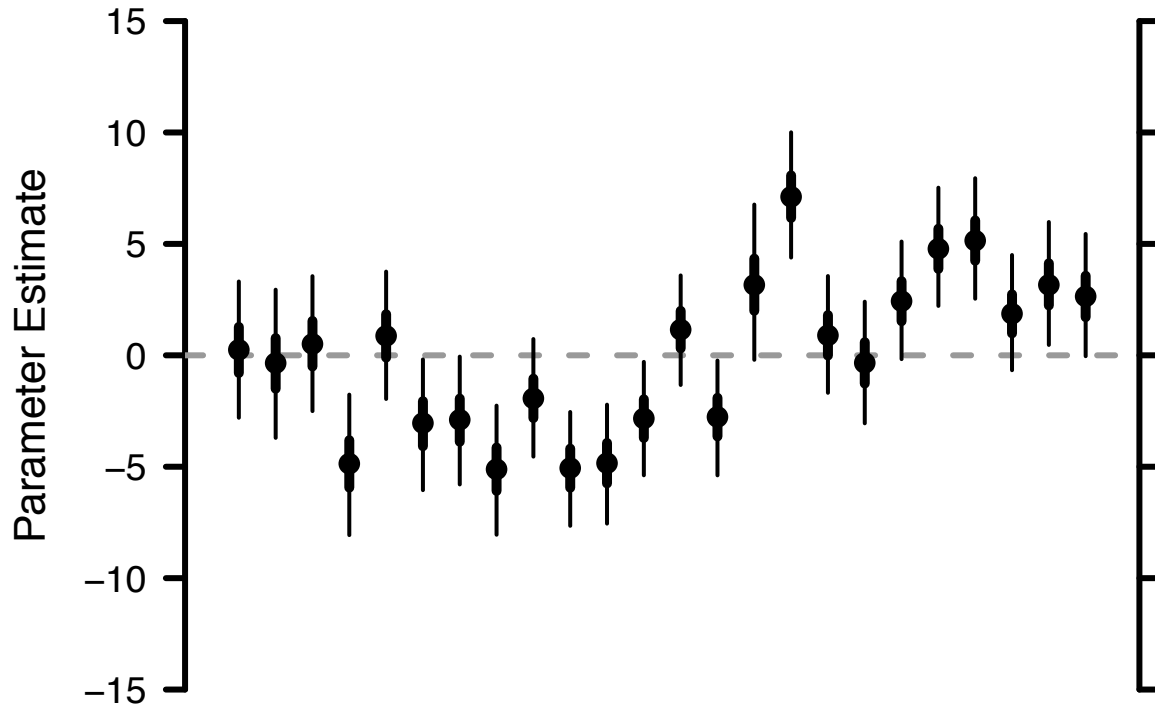
Year effect (alpha)

```

MCMCplot(out,
          params = 'alpha',

```

```
rank = FALSE,
labels = NULL,
horiz = FALSE,
ref_ovl = FALSE,
ylim = c(-15, 15))
```



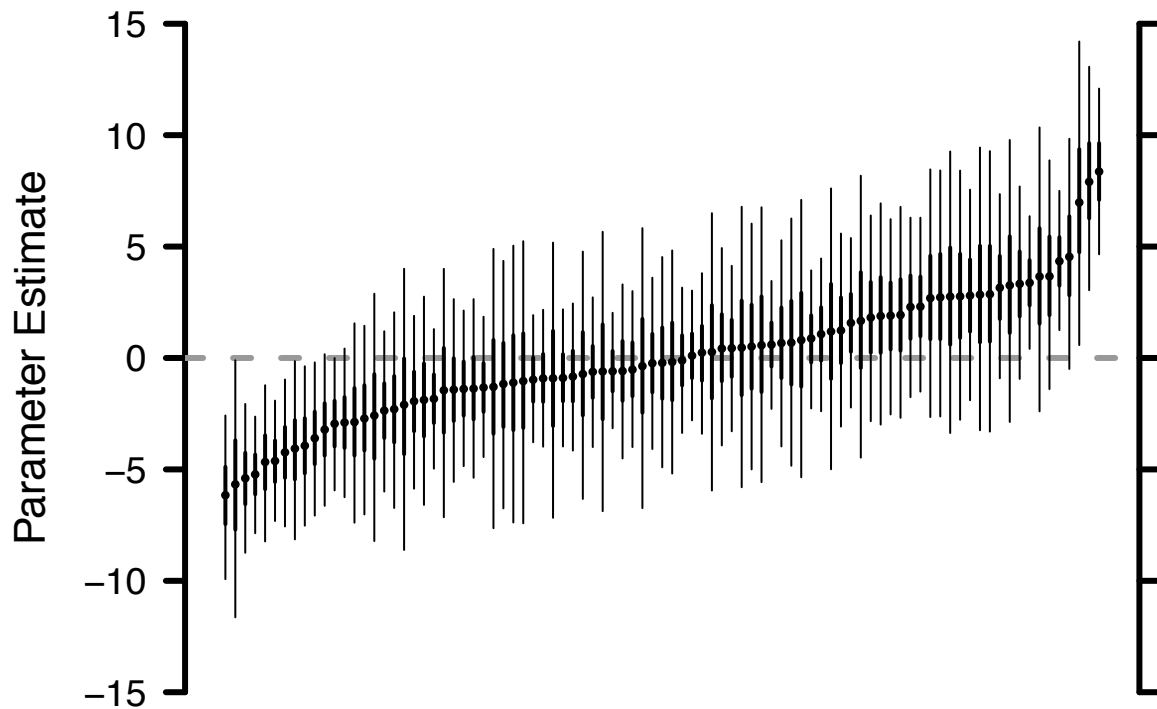
```
MCMCsummary(out,
  params = 'alpha')
```

```
##           mean    sd  2.5%   50%  97.5% Rhat
## alpha[1]  0.24  1.55 -2.80  0.25  3.31    1
## alpha[2] -0.36  1.69 -3.70 -0.35  2.95    1
## alpha[3]  0.52  1.54 -2.50  0.51  3.55    1
## alpha[4] -4.87  1.60 -8.07 -4.86 -1.76    1
## alpha[5]  0.87  1.46 -1.96  0.87  3.76    1
## alpha[6] -3.07  1.50 -6.05 -3.04 -0.18    1
## alpha[7] -2.90  1.45 -5.80 -2.89 -0.06    1
## alpha[8] -5.12  1.47 -8.05 -5.12 -2.26    1
## alpha[9] -1.93  1.33 -4.55 -1.93  0.73    1
## alpha[10] -5.07  1.31 -7.65 -5.06 -2.54    1
## alpha[11] -4.85  1.36 -7.55 -4.84 -2.21    1
## alpha[12] -2.84  1.30 -5.38 -2.84 -0.29    1
## alpha[13]  1.15  1.25 -1.33  1.15  3.59    1
## alpha[14] -2.78  1.30 -5.39 -2.77 -0.23    1
## alpha[15]  3.18  1.76 -0.20  3.16  6.77    1
## alpha[16]  7.13  1.43  4.39  7.11 10.01    1
## alpha[17]  0.90  1.34 -1.68  0.90  3.56    1
## alpha[18] -0.33  1.39 -3.05 -0.34  2.41    1
## alpha[19]  2.44  1.34 -0.17  2.43  5.11    1
## alpha[20]  4.80  1.35  2.22  4.78  7.52    1
## alpha[21]  5.16  1.37  2.54  5.15  7.95    1
```

```
## alpha[22]  1.87 1.31 -0.67  1.87  4.50  1
## alpha[23]  3.19 1.40  0.47  3.16  5.98  1
## alpha[24]  2.65 1.39 -0.04  2.65  5.45  1
```

Individual effect (beta)

```
MCMCplot(out,
  params = 'beta',
  rank = TRUE,
  labels = NULL,
  horiz = FALSE,
  thick_sz = 2,
  thin_sz = 1,
  med_sz = .6,
  ref_ovl = FALSE,
  ylim = c(-15, 15))
```



```
MCMCsummary(out,
  params = 'beta')
```

##		mean	sd	2.5%	50%	97.5%	Rhat
##	beta[1]	2.28	2.07	-1.76	2.29	6.30	1
##	beta[2]	-2.71	2.16	-7.02	-2.72	1.44	1
##	beta[3]	-0.36	3.19	-6.74	-0.37	5.83	1
##	beta[4]	-2.96	1.52	-5.94	-2.95	0.00	1
##	beta[5]	1.74	3.21	-4.47	1.67	8.18	1
##	beta[6]	4.60	2.62	-0.49	4.54	9.83	1
##	beta[7]	8.37	1.90	4.65	8.36	12.09	1
##	beta[8]	-2.18	3.22	-8.61	-2.10	4.00	1
##	beta[9]	-0.23	1.96	-4.09	-0.23	3.60	1
##	beta[10]	-6.18	1.89	-9.93	-6.16	-2.58	1

```

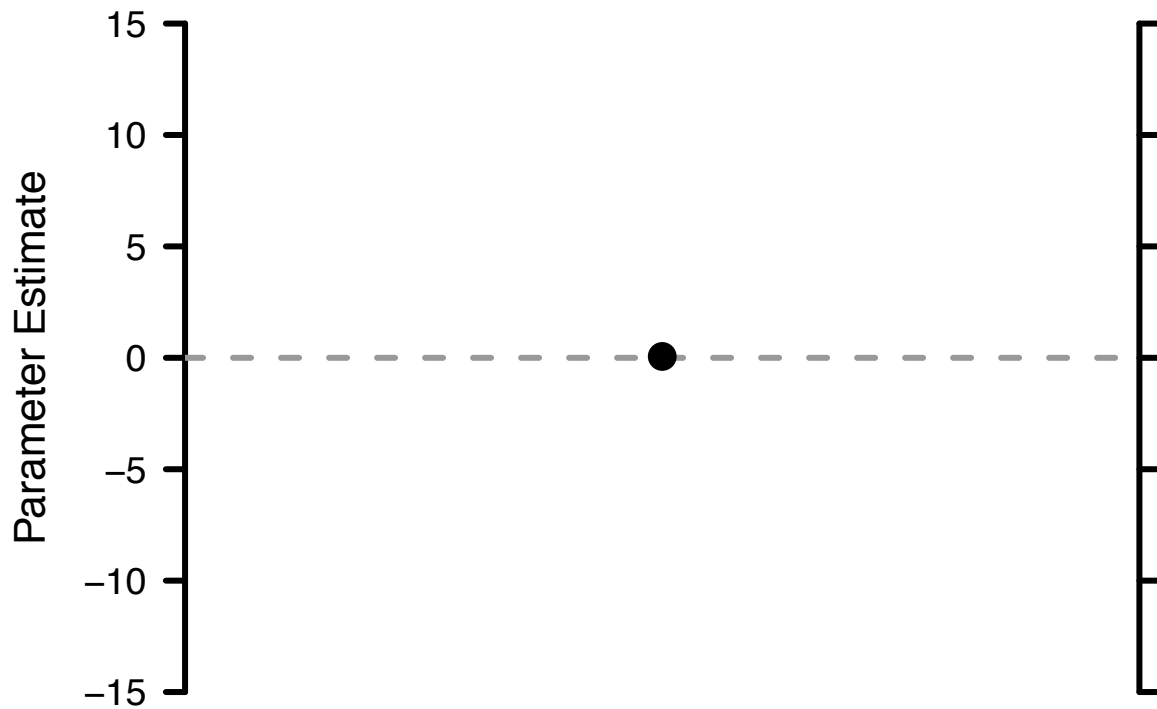
## beta[11] -0.91 1.58 -3.98 -0.92 2.16 1
## beta[12] -1.47 2.83 -7.15 -1.45 4.00 1
## beta[13] 0.86 1.58 -2.27 0.88 3.93 1
## beta[14] -0.51 1.78 -4.00 -0.52 3.00 1
## beta[15] -0.89 1.57 -3.97 -0.89 2.18 1
## beta[16] 1.08 1.76 -2.39 1.07 4.46 1
## beta[17] -1.83 1.61 -4.97 -1.83 1.30 1
## beta[18] -2.88 2.27 -7.39 -2.88 1.56 1
## beta[19] -0.63 1.71 -4.00 -0.62 2.72 1
## beta[20] 2.80 2.40 -1.90 2.80 7.55 1
## beta[21] -3.60 1.75 -7.07 -3.60 -0.20 1
## beta[22] 7.09 3.48 0.58 6.98 14.20 1
## beta[23] 3.69 2.61 -1.40 3.66 8.87 1
## beta[24] 1.22 3.20 -4.99 1.19 7.61 1
## beta[25] -4.63 1.38 -7.32 -4.62 -1.91 1
## beta[26] -0.96 1.45 -3.78 -0.97 1.92 1
## beta[27] 2.80 3.21 -3.37 2.76 9.27 1
## beta[28] -1.12 3.18 -7.38 -1.11 5.04 1
## beta[29] -0.71 2.81 -6.33 -0.72 4.77 1
## beta[30] -1.04 3.21 -7.42 -1.04 5.24 1
## beta[31] -0.58 1.32 -3.15 -0.60 2.03 1
## beta[32] 0.67 2.34 -3.97 0.67 5.28 1
## beta[33] 0.70 2.82 -4.84 0.69 6.26 1
## beta[34] -3.22 1.74 -6.64 -3.21 0.17 1
## beta[35] -1.95 1.98 -5.87 -1.94 1.89 1
## beta[36] -3.95 1.84 -7.52 -3.94 -0.37 1
## beta[37] -4.25 1.69 -7.56 -4.24 -0.97 1
## beta[38] -5.40 1.71 -8.74 -5.40 -2.06 1
## beta[39] -0.93 3.17 -7.17 -0.91 5.18 1
## beta[40] -5.73 2.96 -11.64 -5.67 -0.10 1
## beta[41] -0.10 1.66 -3.37 -0.11 3.16 1
## beta[42] -1.32 1.62 -4.45 -1.33 1.85 1
## beta[43] -4.11 2.01 -8.14 -4.07 -0.14 1
## beta[44] 1.81 2.35 -2.84 1.81 6.40 1
## beta[45] -5.23 1.33 -7.86 -5.22 -2.63 1
## beta[46] 0.26 3.15 -5.95 0.27 6.50 1
## beta[47] 0.10 1.49 -2.80 0.10 3.03 1
## beta[48] 2.89 3.21 -3.30 2.86 9.28 1
## beta[49] 3.71 3.22 -2.39 3.65 10.35 1
## beta[50] 0.22 1.83 -3.40 0.24 3.80 1
## beta[51] 4.34 1.59 1.25 4.34 7.50 1
## beta[52] 0.60 1.47 -2.29 0.60 3.45 1
## beta[53] -2.30 2.23 -6.73 -2.30 2.05 1
## beta[54] -1.32 3.18 -7.64 -1.30 4.89 1
## beta[55] 2.75 2.84 -2.65 2.69 8.46 1
## beta[56] -1.37 2.06 -5.38 -1.37 2.64 1
## beta[57] -2.90 1.69 -6.25 -2.90 0.42 1
## beta[58] 2.79 2.82 -2.77 2.76 8.41 1
## beta[59] 3.37 1.51 0.41 3.38 6.36 1
## beta[60] 2.34 1.99 -1.51 2.31 6.30 1
## beta[61] 2.90 3.24 -3.24 2.84 9.44 1
## beta[62] -1.42 2.10 -5.56 -1.42 2.64 1
## beta[63] -1.20 2.83 -6.75 -1.16 4.36 1
## beta[64] 0.43 1.90 -3.29 0.44 4.13 1

```

```
## beta[65]  1.91 2.55 -2.99  1.88  6.94  1
## beta[66] -2.62 2.83 -8.22 -2.58  2.88  1
## beta[67] -1.38 1.79 -4.85 -1.39  2.13  1
## beta[68]  0.47 3.19 -5.80  0.46  6.79  1
## beta[69]  3.33 3.23 -2.87  3.26  9.78  1
## beta[70]  7.95 2.53  3.04  7.91 13.07  1
## beta[71]  0.45 2.24 -3.92  0.42  4.93  1
## beta[72]  3.34 2.17 -0.94  3.33  7.70  1
## beta[73] -0.16 2.57 -5.19 -0.18  4.83  1
## beta[74] -1.89 2.40 -6.59 -1.88  2.75  1
## beta[75] -0.63 3.19 -6.87 -0.60  5.66  1
## beta[76]  0.51 2.81 -5.00  0.51  6.03  1
## beta[77] -0.22 2.40 -4.91 -0.22  4.53  1
## beta[78]  1.96 2.41 -2.69  1.93  6.78  1
## beta[79]  2.77 2.83 -2.62  2.72  8.42  1
## beta[80] -4.68 1.79 -8.23 -4.67 -1.22  1
## beta[81] -0.82 1.68 -4.15 -0.84  2.45  1
## beta[82]  1.88 2.21 -2.53  1.90  6.23  1
## beta[83]  1.24 2.20 -3.08  1.24  5.58  1
## beta[84]  0.82 3.16 -5.35  0.80  7.10  1
## beta[85]  3.17 2.10 -0.91  3.15  7.35  1
## beta[86] -2.37 1.84 -5.99 -2.36  1.20  1
## beta[87]  0.61 3.16 -5.57  0.57  6.76  1
## beta[88]  1.58 1.94 -2.22  1.57  5.38  1
## beta[89] -0.58 2.00 -4.51 -0.59  3.30  1
```

Age effect (gamma)

```
MCMCplot(out,
  params = 'gamma',
  rank = TRUE,
  labels = NULL,
  horiz = FALSE,
  med_sz = 2,
  ref_ovl = FALSE,
  ylim = c(-15, 15))
```



```
MCMCsummary(out,
  params = 'gamma')
```

```
##      mean  sd  2.5%  50% 97.5% Rhat
## gamma 0.06 0.04 -0.03 0.06  0.15   1
```

Variance estimates (inverse precision)

```
MCMCsummary(out,
  params = c('var.year', 'var.ind', 'var.model'))
```

```
##      mean  sd  2.5%  50% 97.5% Rhat
## var.year 14.83 5.50  7.16 13.81 28.43   1
## var.ind  14.09 3.80  7.95 13.66 22.74   1
## var.model 35.05 2.26 30.92 34.96 39.75   1
```

Skewness test and plots

Captive

```
#scale and aggregate data
```

```
sc_agg_fun <- function(IN)
{
  yrs <- range(IN$YEAR)

  OUT <- c()
  for(i in yrs[1]:yrs[2])
```

```
{
  temp <- filter(IN, YEAR == i)
  s_CID <- scale(temp$J_CID, scale = TRUE)

  t.out <- cbind(temp, s_CID)
  OUT <- rbind(OUT, t.out)
}
return(OUT)
}
```

```
cap_sk <- sc_agg_fun(captive_data)
```

Skew determined using D'Agostino test

```
skew_captive <- agostino.test(cap_sk$s_CID)$statistic[1]
agostino.test(cap_sk$s_CID)
```

```
##
## D'Agostino skewness test
##
## data: cap_sk$s_CID
## skew = 0.54072, z = 5.24950, p-value = 1.525e-07
## alternative hypothesis: data have a skewness
```

Standard error skew

```
#standard error of skewness function
ses <- function(n)
{
  sqrt((6*n*(n-1))/((n-2)*(n+1)*(n+3)))
}
```

```
length_captive <- dim(cap_sk)[1]
```

```
ses(length_captive)
```

```
## [1] 0.09774553
```

Wild

```
wild_sk <- sc_agg_fun(wild_data)
```

Skew

```
skew_wild <- agostino.test(wild_sk$s_CID)$statistic[1]
agostino.test(wild_sk$s_CID)
```

```
##
## D'Agostino skewness test
##
## data: wild_sk$s_CID
## skew = 0.79228, z = 16.09200, p-value < 2.2e-16
## alternative hypothesis: data have a skewness
```

Standard error skew

```
length_wild <- dim(wild_sk)[1]

ses(length_wild)
```

```
## [1] 0.04376183
```

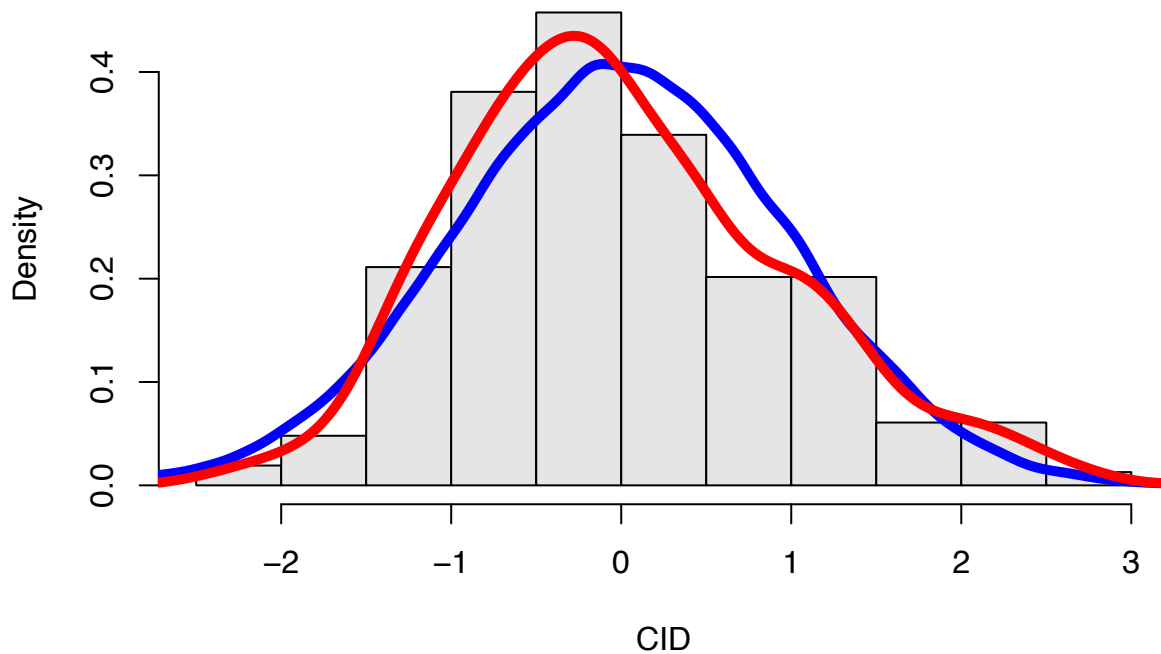
Simulate normal breeding distribution given true CID mean and sd - Plot

Captive

```
m_cap <- mean(cap_sk$s_CID, na.rm = TRUE)
sd_cap <- sd(cap_sk$s_CID, na.rm = TRUE)
cap_rd <- rnorm(100000, mean = m_cap, sd = sd_cap)

hist(cap_sk$s_CID, prob = TRUE,
     main = 'Breeding distribution - Captive',
     xlab = 'CID', ylab = 'Density', col = 'grey90',
     xlim = c(-2.5, 3),
     breaks = 15)
lines(density(cap_rd), col = 'blue', lwd = 5)
lines(density(cap_sk$s_CID, na.rm = TRUE), col = 'red', lwd = 5)
```

Breeding distribution – Captive



Wild

```
m_wild <- mean(wild_sk$s_CID, na.rm=TRUE)
sd_wild <- sd(wild_sk$s_CID, na.rm=TRUE)
wild_rd <- rnorm(100000, mean= m_wild, sd= sd_wild)

hist(wild_sk$s_CID, prob=TRUE,
     main='Breeding distribution - Wild',
```

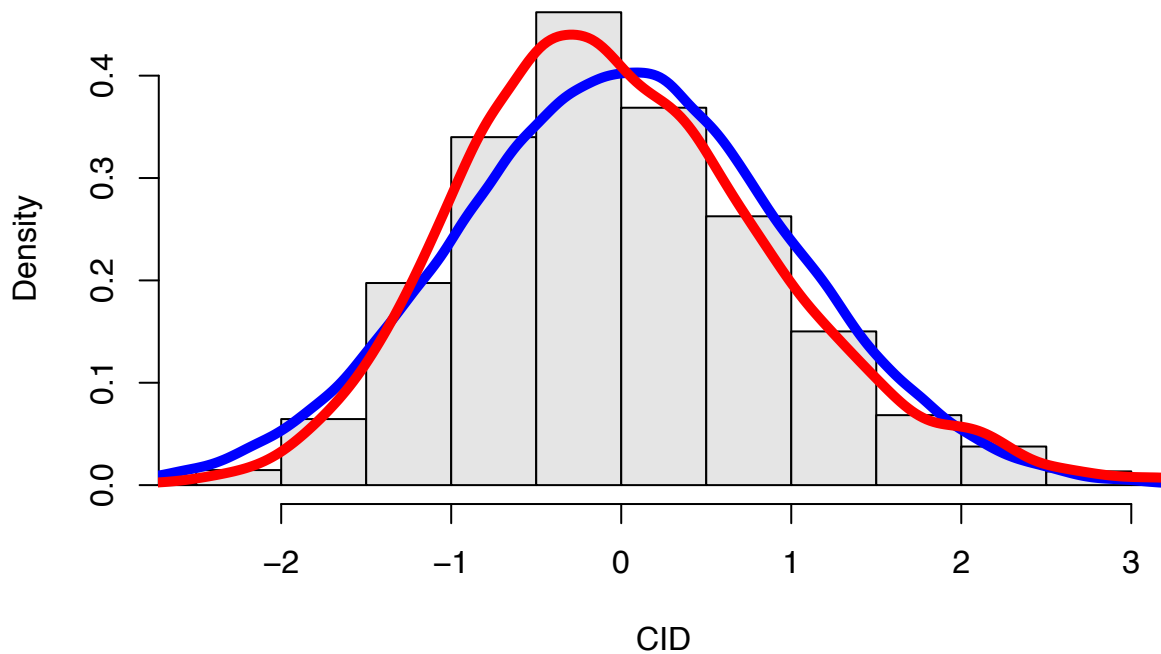


```

xlab= 'CID', ylab= 'Density', col = 'grey90',
xlim = c(-2.5, 3),
breaks = 25)
lines(density(wild_rd), col='blue', lwd=5)
lines(density(wild_sk$s_CID, na.rm=TRUE), col='red', lwd=5)

```

Breeding distribution – Wild



First CID as a predictor for median CID

Fit a linear model to examine the predictive power of first CID for median CID in a given year.

#remove first values when calculating median for that year

```

#CAPTIVE
YRS_C <- unique(captive_data$YEAR)

OUT_C <- c()
for (i in 1:length(YRS_C))
{
  #i <- 1
  temp <- filter(captive_data, YEAR == YRS_C[i])
  min_temp <- min(temp$J_CID)
  min_ind <- which(temp$J_CID == min(temp$J_CID))
  med_temp <- median(temp$J_CID[-min_ind])

  t_OUT_C <- c(YRS_C[i], min_temp, med_temp)
  OUT_C <- rbind(OUT_C, t_OUT_C)
}

```

```

fit_C <- summary(lm(OUT_C[,3] ~ OUT_C[,2]))

#WILD
YRS_W <- unique(wild_data$YEAR)

OUT_W <- c()
for (i in 1:length(YRS_W))
{
  #i <- 1
  temp <- filter(wild_data, YEAR == YRS_W[i])
  min_temp <- min(temp$J_CID)
  min_ind <- which(temp$J_CID == min(temp$J_CID))
  med_temp <- median(temp$J_CID[-min_ind])

  t_OUT_W <- c(YRS_W[i], min_temp, med_temp)
  OUT_W <- rbind(OUT_W, t_OUT_W)
}

fit_W <- summary(lm(OUT_W[,3] ~ OUT_W[,2]))

```

Captive model $r^2 = 0.7$

Wild model $r^2 = 0.7$

Explanatory power is high and very similar between the captive and wild populations.

Skew estimates from literature

Data on skew of phenological data from Thomson 1980, Sparks et al. 2005, Wilson 2013 from plant and bird species. Data is composed of various phenological measures, including first flowering for plants and first arrival for birds (which differs from CID used in this study).

```

setwd('Data')

lit_skew <- read.csv('Lit_skew.csv', header = TRUE)

mn_skew_lit <- mean(lit_skew$Skew)

```

mean skew = 0.43

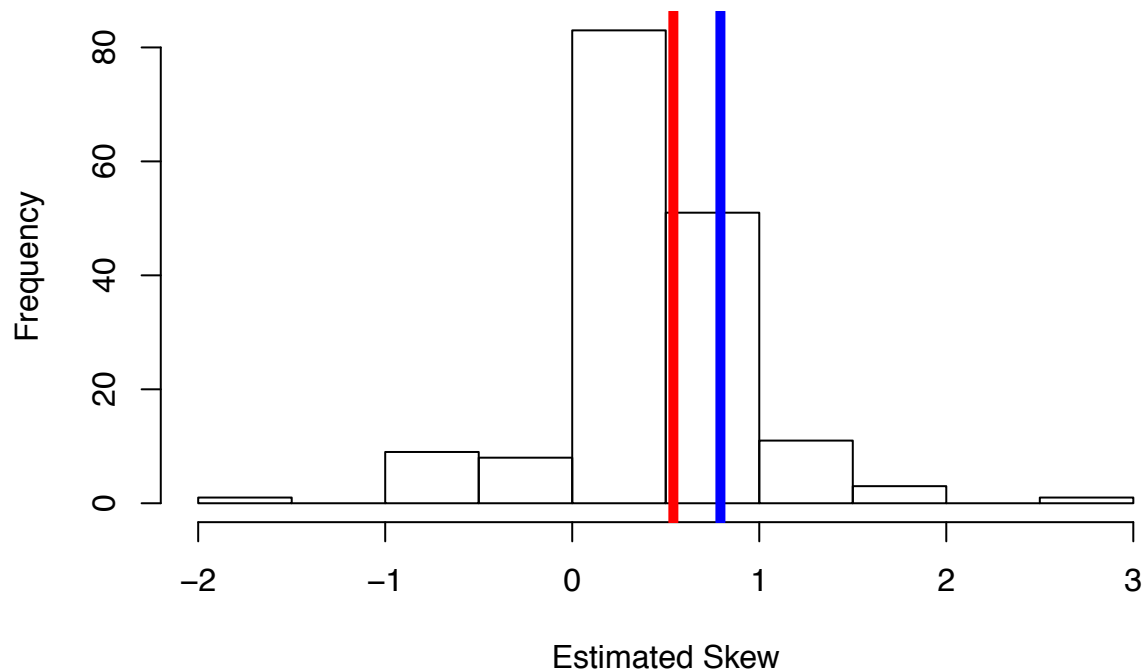
Histogram of skew from literature

```

hist(lit_skew$Skew,
     main = 'Red = Captive; Blue = Wild',
     xlab = 'Estimated Skew')
abline(v = skew_captive, col = 'red', lwd = 5)
abline(v = skew_wild, col = 'blue', lwd = 5)

```

Red = Captive; Blue = Wild



```
per_captive <- length(which(lit_skew$Skew > skew_captive))/NROW(lit_skew)
per_wild <- length(which(lit_skew$Skew > skew_wild))/NROW(lit_skew)
```

Percent literature values greater than captive population skew = 37%

Percent literature values greater than wild population skew = 17%

Skew for Adélie penguin CID is slightly higher than the skew estimated for most populations.

Simulation of right skew breeding distribution

Simple model to show that a right skew distribution can be produced when breeding is accelerated proportional to the number of pairs that have recently initiated breeding.

```
#simulate a normal distirbution (breeding in the absence of conspecifics)
set.seed(1)
time <- round(rnorm(1000, 50, 10))
time <- sort(time)
#no significant skew
agostino.test(time)
```

```
##
## D'Agostino skewness test
##
## data: time
## skew = -0.01578, z = -0.20520, p-value = 0.8374
## alternative hypothesis: data have a skewness
```

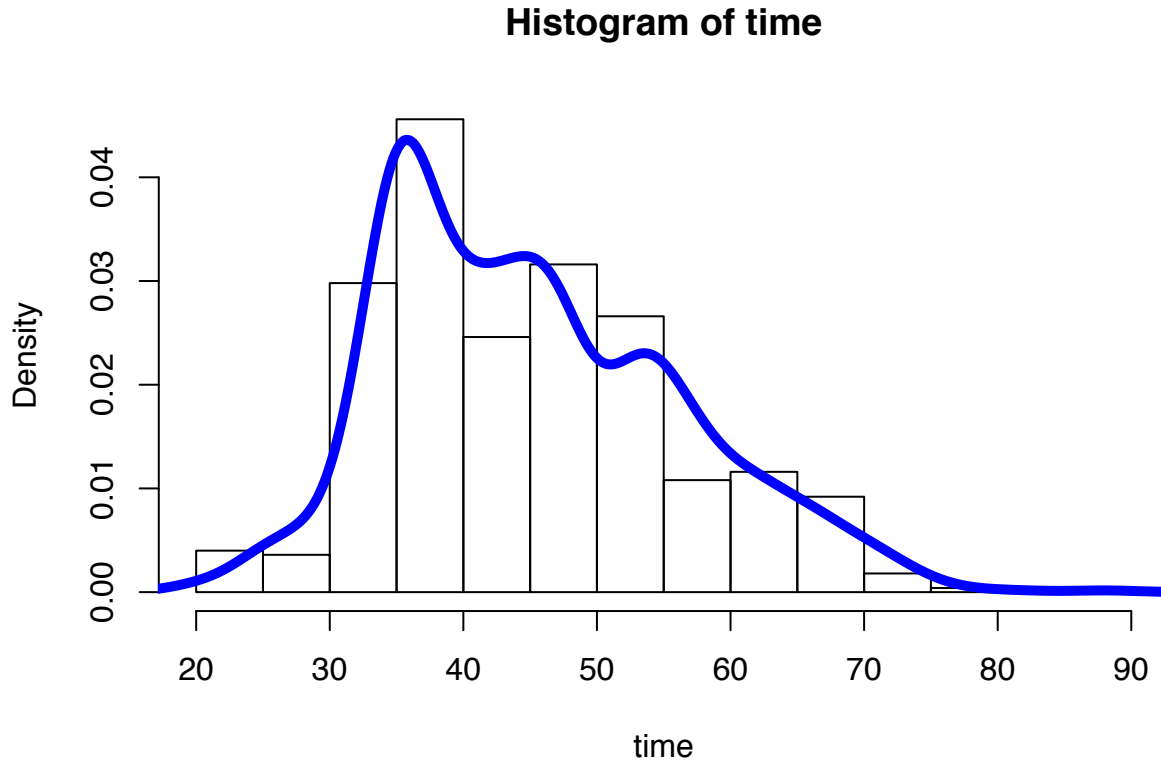
```
#simulate 'contagion effect' of breeding
for (i in min(time):max(time))
{
```

```

time[time == i] <- time[time == i] - sum(as.numeric((time > (i - 3)) & (time < i)))/4
}

hist(time, prob = TRUE)
lines(density(time), col = 'blue', lwd = 5)

```



```

agostino.test(time)

##
## D'Agostino skewness test
##
## data:  time
## skew = 0.55355, z = 6.74630, p-value = 1.516e-11
## alternative hypothesis: data have a skewness

```

Literature Cited

- Both, C., van Asch, M., Bijlsma, R.G., van den Burg, A.B. & Visser, M.E. (2009) Climate change and unequal phenological changes across four trophic levels: constraints or adaptations? *Journal of Animal Ecology*, 78, 73–83.
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Appendix S2: Additional factors that may affect Adélie penguin breeding phenology

Rethinking ‘normal’: The role of stochasticity in the phenology of a synchronously breeding seabird

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The effect of breeding in year t-1 on breeding in year t

We conducted a post-hoc analysis on the captive population data to investigate temporal autocorrelation in the posterior estimates for the year effect (Fig. 2a). Plotting clutch initiation date (CID) in year t against CID in year t-1, the effect of this temporal inertia on CID is apparent (Fig S1).

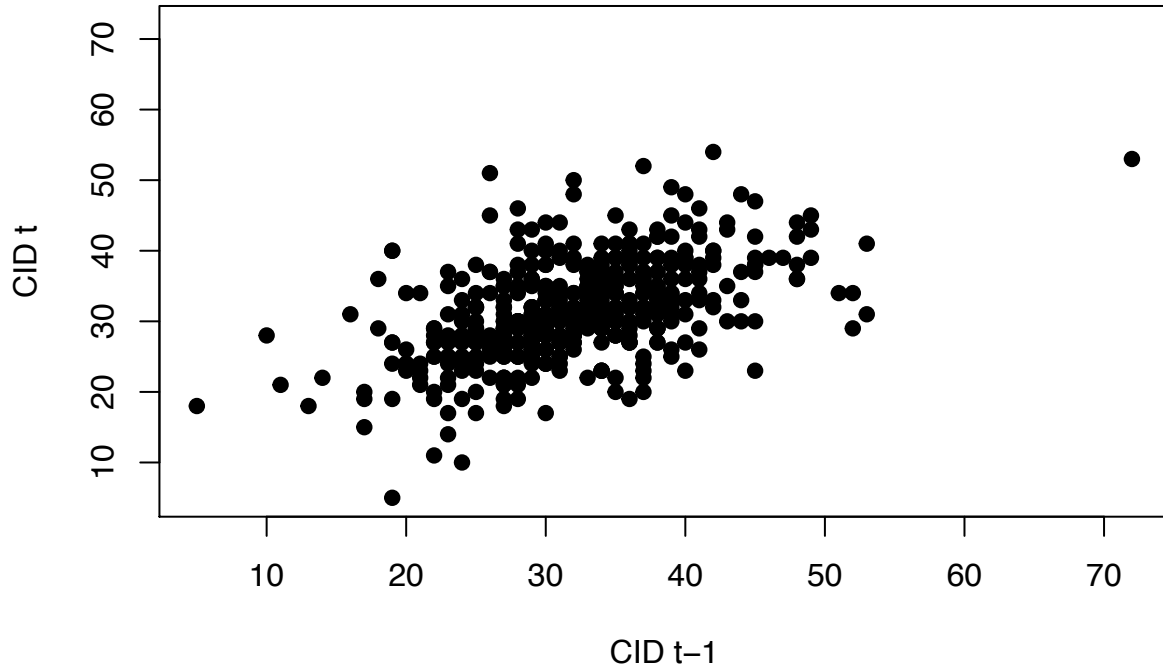


Figure S1: CID for all individuals in the captive population (see Methods) in year t plotted against CID in year t-1 ($r^2 = 0.27$).

To further investigate this pattern, we fit a hierarchical Bayesian model, similar to Eq 1, but with an added autoregressive term, to account for possible temporal autocorrelation.

$$y_{ij} = \mu + \alpha_i + \pi * y_{i-1j} + \beta_j + \gamma * AGE_{ij} + \epsilon_{ij} \quad (S1)$$

$$\alpha_i \sim N(0, \sigma_{year}^2)$$

$$\pi \sim N(0, 1000)$$

$$\beta_j \sim N(0, \sigma_{individual}^2)$$

$$\gamma \sim N(0, 1000)$$

$$\epsilon_{ij} \sim N(0, \sigma_{model}^2)$$

where y_{ij} represents CID, μ represents the intercept, α represents the year effect, β represents the individual effect, π represents the autoregressive term, γ represents the effect of age, AGE represents the age of the female penguin, and ϵ represents the error term.

The model was fit using the R package ‘R2jags’ (Su and Yajima 2015), to interface with JAGS (Plummer 2003) in the R statistical environment (R Development Core Team 2016). Broad Gamma priors were used for all precision ($\tau = \frac{1}{\sigma^2}$) parameters (shape = 0.01, rate = 0.01). Inferences were derived from 20,000 samples drawn following a ‘burn-in’ period of 30,000 draws, using a thinning rate of 2 and 3 chains. Model convergence was assessed through a visual analysis of the posterior chains, in addition to the use of the Gelman-Rubin convergence diagnostic (Brooks and Gelman 1998). All models unambiguously converged. Parameter estimates plots were generated using the ‘MCMCvis’ package (Youngflesh 2016) in the R statistical environment.

RESULTS

Even when accounting for temporal autocorrelation, the year effect appears strong (Fig S2, S3). This suggests that even when controlling for the effect of previous year, the stochastic component to CID across years is still apparent. Inclusion of the autoregressive term does not substantially impact the posterior results of the other parameters. Individual effects are similar between the two models, with estimates closer to 0 when including the autoregressive term (Fig S5, S6). The effect of age is also similar between the two models (Fig S7, S8).

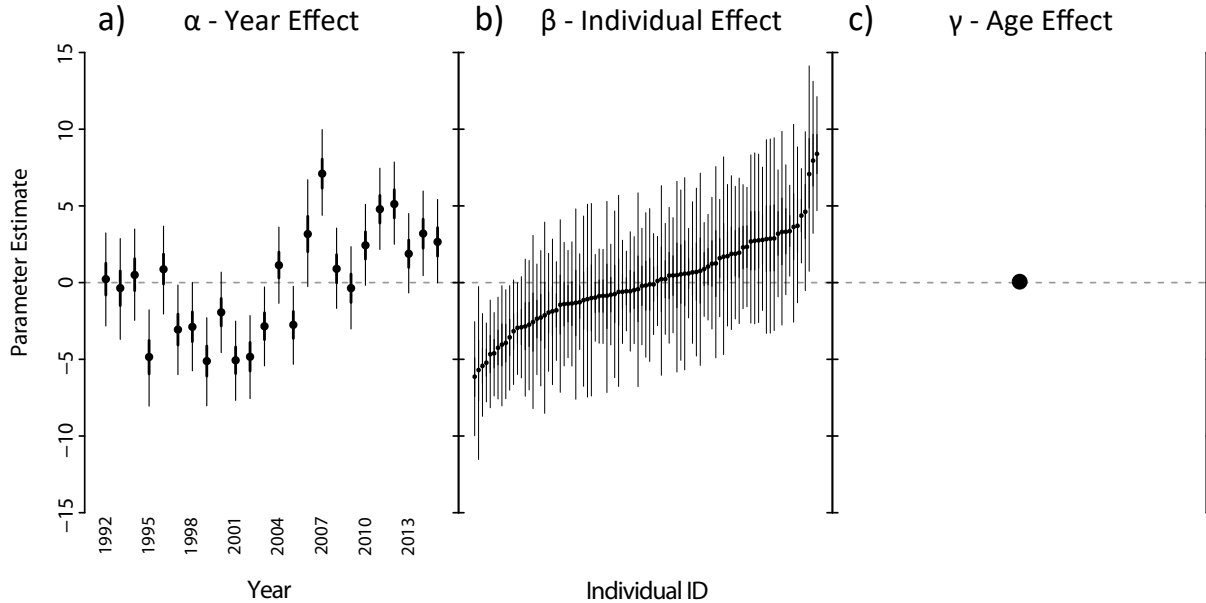


Figure S2: Posterior estimates for the captive population parameters: (a) year effect – α ; (b) individual effect – β ; and (c) age effect – γ parameters for the original model, that does not include the auto-regressive term (see Eq 1). Black circles represent posterior medians. Thicker lines represent 50% credible intervals while thinner lines represent 95% credible intervals. Error bars for the γ parameter are not visible.

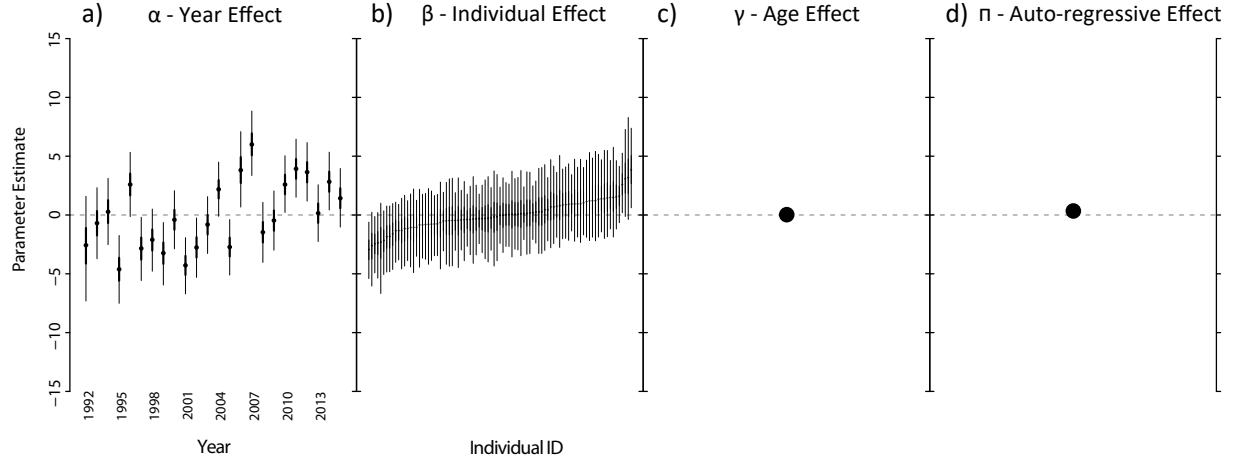


Figure S3: Posterior estimates for the captive population parameters: (a) year effect – α ; (b) individual effect – β ; (c) age effect – γ ; and (d) autoregressive effect – π parameters for the model that includes the auto-regressive term (see Eq S1). Black circles represent posterior medians. Thicker lines represent 50% credible intervals while thinner lines represent 95% credible intervals. Error bars for the γ and π parameters are not visible.

Our primary concern was to determine whether autocorrelation in the CID of individual penguins across years could explain the year effect apparent in the original model (Eq 1). We show that temporal inertia in CID does exist, though it does not explain the year-to-year stochasticity in CID. The reason for this temporal autocorrelation may be due to physiological factors but is beyond the scope of this study. Our model results show a strong year effect in CID is still apparent when accounting for this potentially confounding factor.

The effect of breeding population size on CID

We were also interested to know if the number of breeders in a particular year impacted the breeding phenology of the captive penguins. To further investigate this pattern, we fit a hierarchical Bayesian model, similar to Eq 1, but with an added term for the number of breeders in each year.

$$y_{ij} = \mu + \alpha_i + \beta_j + \gamma * AGE_{ij} + \zeta * NB_i + \epsilon_{ij} \quad (S2)$$

$$\alpha_i \sim N(0, \sigma_{year}^2)$$

$$\beta_j \sim N(0, \sigma_{individual}^2)$$

$$\gamma \sim N(0, 1000)$$

$$\zeta \sim N(0, 1000)$$

$$\epsilon_{ij} \sim N(0, \sigma_{model}^2)$$

where y_{ij} represents CID, μ represents the intercept, α represents the year effect, β represents the individual effect, γ represents the effect of age, AGE represents the age of the female penguin, ζ represents the effect of the number of breeders, NB represents the number of breeders in each year, and ϵ represents the error term.

The model was fit using the same methodology denoted above.

RESULTS

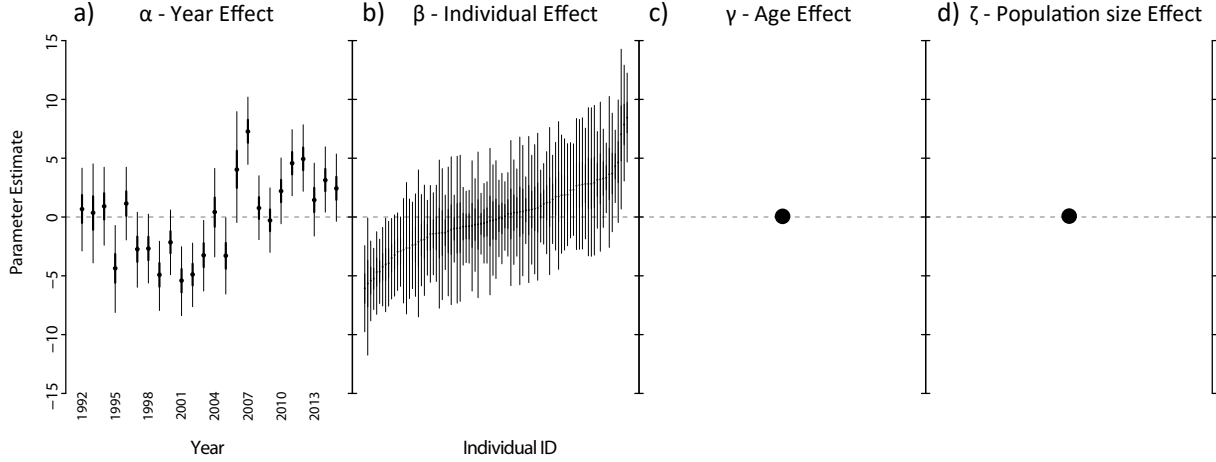


Figure S4: Posterior estimates for the captive population parameters: (a) year effect – α ; (b) individual effect – β ; (c) age effect – γ ; and (d) effect of population size – ζ (see Eq S2). Black circles represent posterior medians. Thicker lines represent 50% credible intervals while thinner lines represent 95% credible intervals. Error bars for the γ and ζ parameters are not visible.

It does not appear that population size has a strong effect on captive penguin CID. The parameter estimate for ζ is small and a year-effect is still apparent.

The effect of the timing of nesting material availability on breeding phenology

We initially hypothesized that the timing of nesting material availability may also impact CID. Adélie penguin rely on the availability of stones to build nests before laying eggs during the breeding season. We compared the ‘waiting time’ of a wild Adélie penguin population at Cape Crozier (77.45°S, 169.20°E) (i.e., the time between the first arrival at the colony and the first clutch initiation date [data presented in Table 3.2 of Ainley et al. (1983)]), to the ‘waiting time’ of the captive population (i.e., the time between when nesting materials are first made available to the penguins [available for 2007-2015] and the first clutch initiation date).

Mean time between the first arrival at the colony and the first egg laid in a wild population was found to be 13.7 days (Ainley et al. 1983).

Mean time between when nesting materials first became available and the first egg laid in this captive population was found to be 41.3 days.

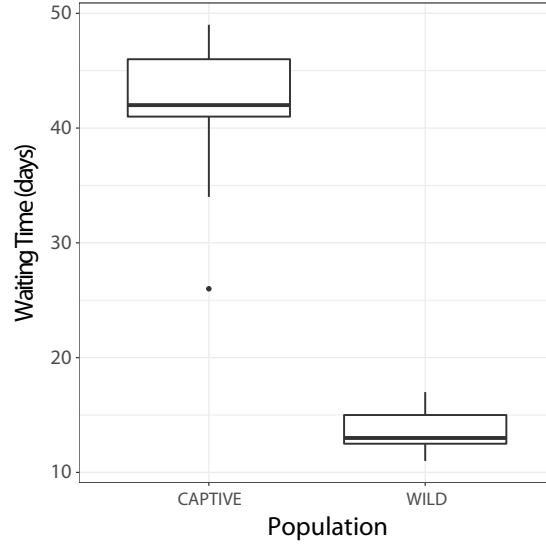


Figure S5: Barchart showing distribution of waiting times for both the captive Adélie penguin population (time between first availability of nesting materials and first CID) and the wild Adélie penguin population observed by Ainley et al. (1983) (time between first arrival at the colony and first CID). This analysis was conducted using the mean CID in the captive population as opposed to the min CID with the same results.

The mean waiting time is more than 3 times higher in captivity than the wild. This suggests that availability of nesting materials is not a barrier for breeding for Adélie penguins in captivity.

Potential effects of 2005 exhibit renovation on phenology

CID appears slightly delayed following the captive exhibit renovation in 2005. To investigate whether this impacted our results, we standardized median CID for 1992-2004 and from 2006-2015 (removing 2005 to account for any impact that the renovation may have had in that year), and calculated the variance for the time series.

To further investigate the effect that any potential step-change due to the 2005 renovation may have had on CID, we fit a hierarchical Bayesian model, similar to Eq 1, but with an added term for pre- and post-renovation identity.

$$y_{ij} = \mu + \alpha_i + \beta_j + \gamma * AGE_{ij} + \kappa_l * RID_i + \epsilon_{ij} \quad (S3)$$

$$\alpha_i \sim N(0, \sigma_{year}^2)$$

$$\beta_j \sim N(0, \sigma_{individual}^2)$$

$$\gamma \sim N(0, 1000)$$

$$\kappa_l \sim N(0, 1000)$$

$$\epsilon_{ij} \sim N(0, \sigma_{model}^2)$$

where y_{ij} represents CID, μ represents the intercept, α represents the year effect, β represents the individual effect, γ represents the effect of age, AGE represents the age of the female penguin, κ represents the effect of pre/post renovation identity, RID represents whether a particular year belongs in the pre or post renovation period, and ϵ represents the error term.

The model was fit using the same methodology denoted above.

RESULTS

$$\sigma_{RID}^2 = 7.59$$

$$\sigma_{AdmiraltyBay}^2 = 13.5$$

When standardizing the pre and post renovation periods, the overall variance of the captive time series decreases, leading to a slightly lower variance than that seen at Admiralty Bay. This is well within the range of variance in CID found at other wild Adélie penguin colonies in Antarctica (Youngflesh et al. 2017), however, confirming that variance in CID in this captive population is as great as that seen in the wild.

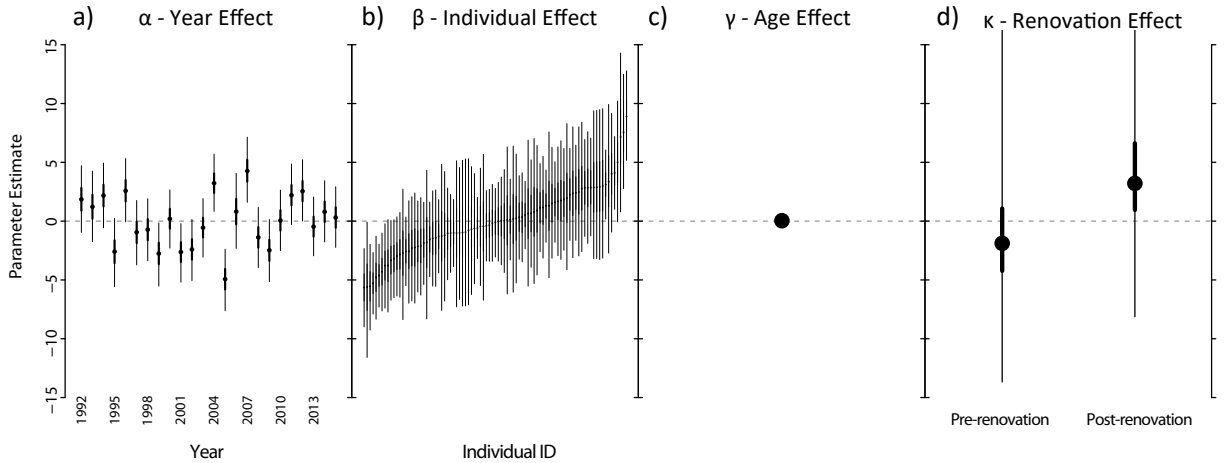


Figure S6: Posterior estimates for the captive population parameters: (a) year effect – α ; (b) individual effect – β ; (c) age effect – γ ; and (d) effect of period id (pre/post renovation) – κ (see Eq S3). Black circles represent posterior medians. Thicker lines represent 50% credible intervals while thinner lines represent 95% credible intervals. Error bars for the γ parameter are not visible.

None of the factors examined changed our overall conclusions. Year effects are slightly weaker when adding the κ term compared to the original model (Fig S2), however are still prominent. Parameter estimates for κ are relatively close to zero, with large credible intervals. Even when accounting for any potential effect that the renovation may have had on CID, interannual variability in CID appears to be the norm.

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